Comment Sheet

APPLICATION SERIAL NUMBER
10/732859

DOES NOT COMPLY WITH THE SEQUENCE RULES. See reasons below.

The computer readable form contains errors. See the attached Raw Sequence Listing Error Report.

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
form:

Application Serial Number: _10/732, 859 A_

Source: _IFW16_

Date Processed by STIC: _11/18/2005_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE
   APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
   NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE __CHECKER
VERSION 4.2.2 PROGRAM__, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
       http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is
a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the
United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission
   User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
   U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street,
   Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10/732,859 A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ____ Variable Length

Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7 ____ Skipped Sequences
(OLD RULES)

Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ.ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____ Skipped Sequences
(NEW RULES)

Sequence(s) _7_ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ____ Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ____ Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ____ Use of <220>

~~Sequence(s) ____ missing the <220> "Feature" and associated numeric identifiers and responses.~~ Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29611-32) (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n/Xaa

"n" can only represent a single <u>nucleotide</u>; "Xaa" can only represent a single <u>amino acid</u>
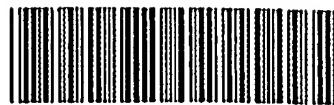
IFW16

RAW SEQUENCE LISTING   DATE: 11/18/2005
PATENT APPLICATION: US/10/732,859A   TIME: 10:02:28

Input Set : A:\10.732859 Sequence Listing (13101.48202).txt
Output Set: N:\CRF4\11182005\J732859A.raw

```
 3 <110> APPLICANT: Turck, Jutta
 4          Archer, John
 6 <120> TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN EUKARYOTES
 8 <130> FILE REFERENCE: 13101/48202
10 <140> CURRENT APPLICATION NUMBER: US 10/732,859A
11 <141> CURRENT FILING DATE: 2003-12-09
13 <150> PRIOR APPLICATION NUMBER: UK 9828660.2
14 <151> PRIOR FILING DATE: 1998-12-24
16 <150> PRIOR APPLICATION NUMBER: US 09/469,211
17 <151> PRIOR FILING DATE: 1999-12-22
19 <160> NUMBER OF SEQ ID NOS: 19
21 <170> SOFTWARE: PatentIn version 3.3
```

Does Not Comply
Corrected Diskette Needed

(pg 1-2)

ERRORED SEQUENCES

```
E--> 1133 <210>   7 (Insert)
E--> 1134 <211>                do not include these in
E--> 1135 <212>                an intentionally skipped sequences.
W--> 1136 <213>                See item #8 on Error Summary
E--> 1138 <400>                                        sheet.
W--> 1140 000
E/S 1143 <210> SEQ ID NO: 8
     1275 <210> SEQ ID NO: 19
     1276 <211> LENGTH: 470
     1277 <212> TYPE: DNA
     1278 <213> ORGANISM: Artificial Sequence
     1280 <220> FEATURE:
     1281 <223> OTHER INFORMATION: Chimeric promoter
     1283 <400> SEQUENCE: 19
     1284 catgcctgca ggtcaacatg gtggagcacg acactctcgt ctactccaag aatatcaaag    60
     1286 atacagtctc agaagaccag agggctattg agactttca acaaagggta atatcgggaa   120
     1288 acctcctcgg attccattgc ccagctatct gtcacttcat cgaaaggaca gtagaaaagg   180
     1290 aagatggctt ctacaaatgc catcattgcg ataaaggaaa ggctatcgtt caagaatgcc   240
     1292 tctaccgaca gtggtcccaa agatgtaccc ccacccacga ggaacatcgt ggaaaaagaa   300
     1294 gacgttccaa ccacgtcttc aaagcaagtg gattgatgtg atatctccac tgacgtaagg   360
     1296 gatgacgcac aatcccacta tccttcgcaa gacccttcct ctatataagt agcgtctgaa   420
     1298 ctagacgtct agcattctag ttgaggaagt tcatttcatt tggagaggac               470
E--> 1301  2/23
E--> 1303  1/23          Pls delete
```

```
<210>  8
<211>  27
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  (OHPR3)
<400>  8
atcgaattcg gatccatgac caccacc
```

→ Insufficient Response. Give Source of Genetic Material See Item # 11 on Error Summary Sheet.

Above is the sample of the similarly Errored Responses.

VERIFICATION SUMMARY   DATE: 11/18/2005
PATENT APPLICATION: US/10/732,859A   TIME: 10:02:29

Input Set : **A:\10.732859 Sequence Listing (13101.48202).txt**
Output Set: **N:\CRF4\11182005\J732859A.raw**

```
L:1133 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:1134 M:210 E: (40) Invalid Number of Sequences, LENGTH:
L:1135 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:0
L:1136 M:201 W: Mandatory field data missing, <213> ORGANISM
L:1138 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:7
L:1140 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (7) SEQUENCE:
L:1143 M:216 E: (34) Seq.#s missing, SEQ ID NOS: 1 thru 7
L:1301 M:254 E: No. of Bases conflict, LENGTH:Input:23 Counted:471 SEQ:19
L:1301 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:1303 M:254 E: No. of Bases conflict, LENGTH:Input:23 Counted:472 SEQ:19
L:1303 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:1303 M:252 E: No. of Seq. differs, <211> LENGTH:Input:470 Found:472 SEQ:19
```